This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (cancelled)

2. (cancelled)

3. (cancelled)

4. (cancelled)

5. (cancelled)

6. (cancelled)

7. (cancelled)

8. (cancelled)

9. (cancelled)

10. (cancelled)

11. (currently amended) A method for removing or controlling errors in nucleic acid molecules comprising arbitrary user-specified sequence composition and length, the method comprising:

a) providing a plurality or pool of nucleic acid molecules, the nucleic acid molecules being synthesized to have a user-specified sequence and length by the steps of:

providing a first immobilized nucleic acid comprising a first 5' region and a first 3' region;

providing at least a second immobilized nucleic acid comprising a second 5' region and a second 3' region, wherein said second 3' region and said first 5' region comprise identical nucleic acid sequences;

contacting said first immobilized nucleic acid with an oligonucleotide under conditions promoting hybridization of said oligonucleotide to said first 3' region and extension of said hybridized oligonucleotide to produce a first extension product comprising a first extension product 3' region that is complementary to said first 5' region; and

contacting said second immobilized nucleic acid with said first extension product under conditions promoting hybridization of said first extension product 3' region to said second 3' region and extension of said hybridized extension product 3' region to produce a second extension product comprising a second extension product 3' region that is complementary to said second 5' region, wherein said second extension product comprises said complementary first and second 3' and 5' regions, and said nucleic acid molecule comprises said second extension product;[[,]] and[[;]]

b) selectively amplifying error-free nucleic acid molecules from said plurality or pool, thereby decreasing the relative amount of any nucleic acid molecules that contain errors.

12. (currently amended) A method for removing or controlling errors in nucleic acid molecules comprising arbitrary user-specified sequence composition and length, the method comprising:

a) providing a plurality or pool of nucleic acid molecules, the nucleic acid molecules being synthesized to have a user-specified sequence and length by the steps of:

providing a first immobilized nucleic acid comprising a first 5' region and a first 3' region;

providing at least a second immobilized nucleic acid comprising a second 5' region and a second 3' region, wherein said second 3' region and said first 5' region comprise identical nucleic acid sequences;

contacting said first immobilized nucleic acid with an oligonucleotide under conditions promoting hybridization of said oligonucleotide to said first 3' region and extension of said hybridized oligonucleotide to produce a first extension product comprising a first extension product 3' region that is complementary to said first 5' region; and

contacting said second immobilized nucleic acid with said first extension product under conditions promoting hybridization of said first extension product 3' region to said second 3' region and extension of said hybridized extension product 3' region to produce a second extension product comprising a second extension product 3' region that is complementary to said second 5' region, wherein said second extension product comprises said complementary first and second 3' and 5' regions, and said nucleic acid molecule comprises said second extension product;[[,]] and[[;]]

b) correcting errors in said plurality or pool using nucleic acid molecules in said plurality or pool as a template for nucleic acid repair.

13. (currently amended) A method for removing or controlling errors in nucleic acid molecules comprising arbitrary user-specified sequence composition and length, the method comprising:

a) providing a plurality or pool of nucleic acid molecules, the nucleic acid molecules being synthesized to have a user-specified sequence and length by the steps of:

providing a first immobilized nucleic acid comprising a first 5' region and a first 3' region;

providing at least a second immobilized nucleic acid comprising a second 5' region and a second 3' region, wherein said second 3' region and said first 5' region comprise identical nucleic acid sequences;

contacting said first immobilized nucleic acid with an oligonucleotide under conditions promoting hybridization of said oligonucleotide to said first 3' region and extension of said hybridized oligonucleotide to produce a first extension product comprising a first extension product 3' region that is complementary to said first 5' region; and

contacting said second immobilized nucleic acid with said first extension product under conditions promoting hybridization of said first extension product 3' region to said second 3' region and extension of said hybridized extension product 3' region to produce a second extension product comprising a second extension product 3' region that is complementary to said second 5' region, wherein said second extension product comprises said complementary first and second 3' and 5' regions, and said nucleic acid molecule comprises said second extension product;[[,]] and[[;]]

b) removing errors from portions of said nucleic acid molecules and recombining remaining portions of said nucleic acid molecules to yield nucleic acid molecules having an error-free sequence.

14. (previously presented) The method of claim 11, further comprising the step of combining at least one error-containing nucleic acid molecule from said plurality or pool with at least one component that prevents amplification of the error-containing nucleic acid molecule.

15. (previously presented) The method of claim 14, wherein the component is a mismatch binding protein.

16. (previously presented) The method of claim 14, wherein the component is cross-linked to the error-containing nucleic acid molecule.

17. (cancelled)

18. (cancelled)

19. (previously presented) The method of claim 14, wherein the component comprises more than one molecule.

20. (withdrawn) The method of claim 12, the step of correcting errors comprising the step of targeting errors via methylation and selective demethylation.

21. (previously presented) The method of claim 12, the step of correcting errors comprising the step of mismatch recognition and cleavage.

22. (previously presented) The method of claim 21, wherein the step of mismatch recognition and cleavage is performed by a resolvase, a single-stranded nuclease, or a combination of a mismatch binding protein and a nuclease.

23. (withdrawn) The method of claim 12, the step of correcting errors comprising the step of generating at least one repair template by disassociation and reassociation of single-stranded nucleic acid molecules.

24. (withdrawn) The method of claim 12, the step of correcting errors comprising the step of generating at least one repair template by strand invasion.

25. (withdrawn) The method of claim 12, wherein no entire nucleic acid molecules in the plurality or pool need be error-free.

26. (previously presented) The method of claim 13, the step of removing errors comprising the step of mismatch recognition and cleavage.

27. (previously presented) The method of claim 26, wherein the step of mismatch recognition and cleavage is performed by a resolvase, a single-stranded nuclease, or a combination of a mismatch binding protein and a nuclease.

28. (withdrawn) The method of claim 26, wherein the step of mismatch recognition and cleavage is performed by a single molecule.

29. (previously presented) The method of claim 13, wherein the step of removing errors is performed by the separate action of a mismatch binding protein and a nuclease.

30. (previously presented) The method of claim 13, wherein no nucleic acid molecules in the plurality or pool need be error-free.